



amdt a

SEQUENCE LISTING

<110> Wood, Clive
Chaudhary, Divya
Long, Andrew
Genetics Institute, Inc.

<120> TRADE MOLECULES, AND USES RELATED THERETO

<130> 22058-569

<140> 09/780,532

<141> 2001-02-09

<150> 60/181,922

<151> 2000-02-11

<150> 60/182,148

<151> 2000-02-14

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 1660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1251)

<400> 1

atg	gct	tta	aaa	gtg	cta	cta	gaa	caa	gag	aaa	acg	ttt	ttc	act	ctt	48
Met	Ala	Leu	Lys	Val	Leu	Leu	Glu	Gln	Glu	Lys	Thr	Phe	Phe	Thr	Leu	
1				5					10					15		

tta	gta	tta	cta	ggc	tat	ttg	tca	tgt	aaa	gtg	act	tgt	gaa	tca	gga	96
Leu	Val	Leu	Leu	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Ser	Gly	
			20					25					30			

gac	tgt	aga	cag	caa	gaa	ttc	agg	gat	cgg	tct	gga	aac	tgt	gtt	ccc	144
Asp	Cys	Arg	Gln	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro	
		35					40					45				

tgc	aac	cag	tgt	ggg	cca	ggc	atg	gag	ttg	tct	aag	gaa	tgt	ggc	ttc	192
Cys	Asn	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	
	50					55					60					

ggc	tat	ggg	gag	gat	gca	cag	tgt	gtg	acg	tgc	cgg	ctg	cac	agg	ttc	240
Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	
65					70				75						80	

aag	gag	gac	tgg	ggc	ttc	cag	aaa	tgc	aag	ccc	tgt	ctg	gac	tgc	gca	288
Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	
			85					90						95		

gtg	gtg	aac	cgc	ttt	cag	aag	gca	aat	tgt	tca	gcc	acc	agt	gat	gcc	336
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
		100						105					110			
atc	tgc	ggg	gac	tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	384
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
		115					120					125				
ggc	ttt	caa	gac	atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	432
Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
	130					135					140					
tac	gaa	ccg	cac	tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	480
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
acg	gcc	tcc	agc	cca	cgg	gac	acg	gcg	ctg	gct	gcc	ggt	atc	tgc	agc	528
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
				165					170					175		
gct	ctg	gcc	acc	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	576
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
tgt	aag	aga	cag	ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	624
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
cag	gac	att	cag	tac	aac	ggc	tct	gag	ctg	tcg	tgt	ttt	gac	aga	cct	672
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Arg	Pro	
	210					215					220					
cag	ctc	cac	gaa	tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	720
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230				235						240	
tca	gtg	cag	acc	tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	768
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245				250						255		
gag	gag	gcc	tgc	agc	ccc	aac	ccg	gcg	act	ctt	ggt	tgt	ggg	gtg	cat	816
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
			260					265					270			
tct	gca	gcc	agt	ctt	cag	gca	aga	aac	gca	ggc	cca	gcc	ggg	gag	atg	864
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
gtg	ccg	act	ttc	ttc	gga	tcc	ctc	acg	cag	tcc	atc	tgt	ggc	gag	ttt	912
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
	290					295					300					
tca	gat	gcc	tgg	cct	ctg	atg	cag	aat	ccc	atg	ggt	ggt	gac	aac	atc	960
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310					315					320	

tct ttt tgt gac tct tat cct gaa ctc act gga gaa gac att cat tct 1008
 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
 325 330 335

ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt 1056
 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
 340 345 350

caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac 1104
 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
 355 360 365

ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa 1152
 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
 370 375 380

tca gca tca act cag gat gca cta act atg aga agc cag cta gat cag 1200
 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
 385 390 395 400

gag agt ggc gct atc atc cac cca gcc act cag acg tcc ctc cag gaa 1248
 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
 405 410 415

gct taaagaacct gcttctttct gcagtagaag cgtgtgctgg aacccaaaga 1301
 Ala

gtactccttt gttaggctta tggactgagc agtctggacc ttgcatggct tctggggcaa 1361

aaatgaatct gaaccaaact gacggcattt gaagcctttc agccagttgc ttctgagcca 1421

gaccagctgt aagctgaaac ctcaatgaat aacaagaaaa gactccaggc cgactcatga 1481

tactctgcat ttttcctaca tgagaagctt ctctgccaca aaagtgactt caaagacgga 1541

tgggttgagc tggcagccta tgagattgtg gacatataac aagaaacaga aatgccctca 1601

tgcttatattt catggtgatt gtggttttac aagactgaag acccagagta tacttttttc 1660

<210> 2
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
 1 5 10 15

Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
 20 25 30

Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
 35 40 45

Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60

Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	
65					70					75					80	
Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	
				85					90					95		
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
			100					105					110			
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
		115					120					125				
Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
	130					135					140					
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
				165					170					175		
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Arg	Pro	
	210					215					220					
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230				235						240	
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245					250					255		
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
			260					265					270			
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
	290					295					300					
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310					315					320	
Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	Ser	
				325					330					335		
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	
			340					345					350			
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	
	355						360					365				

Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu
370						375					380				
Ser	Ala	Ser	Thr	Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	Gln
385					390					395					400
Glu	Ser	Gly	Ala	Ile	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	Glu
				405					410					415	

Ala

<210> 3
 <211> 1325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1269)

<400> 3																
atg	gct	tta	aaa	gtg	cta	cta	gaa	caa	gag	aaa	acg	ttt	ttc	act	ctt	48
Met	Ala	Leu	Lys	Val	Leu	Leu	Glu	Gln	Glu	Lys	Thr	Phe	Phe	Thr	Leu	
1				5					10					15		
tta	gta	tta	cta	ggc	tat	ttg	tca	tgt	aaa	gtg	act	tgt	gaa	aca	gga	96
Leu	Val	Leu	Leu	Gly	Tyr	Leu	Ser	Cys	Lys	Val	Thr	Cys	Glu	Thr	Gly	
			20					25					30			
gac	tgt	aga	cag	caa	gaa	ttc	agg	gat	cgg	tct	gga	aac	tgt	gtt	ccc	144
Asp	Cys	Arg	Gln	Gln	Glu	Phe	Arg	Asp	Arg	Ser	Gly	Asn	Cys	Val	Pro	
		35					40					45				
tgc	aac	cag	tgt	ggg	cca	ggc	atg	gag	ttg	tct	aag	gaa	tgt	ggc	ttc	192
Cys	Asn	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	
	50					55					60					
ggc	tat	ggg	gag	gat	gca	cag	tgt	gtg	acg	tgc	cgg	ctg	cac	agg	ttc	240
Gly	Tyr	Gly	Glu	Asp	Ala	Gln	Cys	Val	Thr	Cys	Arg	Leu	His	Arg	Phe	
65					70					75					80	
aag	gag	gac	tgg	ggc	ttc	cag	aaa	tgc	aag	ccc	tgt	ctg	gac	tgc	gca	288
Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	
			85					90					95			
gtg	gtg	aac	cgc	ttt	cag	aag	gca	aat	tgt	tca	gcc	acc	agt	gat	gcc	336
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
		100					105						110			
atc	tgc	ggg	gac	tgc	ttg	cca	gga	ttt	tat	agg	aag	acg	aaa	ctt	gtc	384
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
	115						120					125				
ggc	ttt	caa	gac	atg	gag	tgt	gtg	cct	tgt	gga	gac	cct	cct	cct	cct	432

Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
130						135					140					
tac	gaa	ccg	cac	tgt	gcc	agc	aag	gtc	aac	ctc	gtg	aag	atc	gcg	tcc	480
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
acg	gcc	tcc	agc	cca	cgg	gac	acg	gcg	ctg	gct	gcc	gtt	atc	tgc	agc	528
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
				165					170					175		
gct	ctg	gcc	acc	gtc	ctg	ctg	gcc	ctg	ctc	atc	ctc	tgt	gtc	atc	tat	576
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
tgt	aag	aga	cag	ttt	atg	gag	aag	aaa	ccc	agc	tgg	tct	ctg	cgg	tca	624
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
cag	gac	att	cag	tac	aac	ggc	tct	gag	ctg	tcg	tgt	ctt	gac	aga	cct	672
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Leu	Asp	Arg	Pro	
	210					215					220					
cag	ctc	cac	gaa	tat	gcc	cac	aga	gcc	tgc	tgc	cag	tgc	cgc	cgt	gac	720
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230				235						240	
tca	gtg	cag	acc	tgc	ggg	ccg	gtg	cgc	ttg	ctc	cca	tcc	atg	tgc	tgt	768
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245					250					255		
gag	gag	gcc	tgc	agc	ccc	aac	ccg	gcg	act	ctt	ggt	tgt	ggg	gtg	cat	816
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
			260					265					270			
tct	gca	gcc	agt	ctt	cag	gca	aga	aac	gca	ggc	cca	gcc	ggg	gag	atg	864
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
gtg	ccg	act	ttc	ttc	gga	tcc	ctc	acg	cag	tcc	atc	tgt	ggc	gag	ttt	912
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
	290					295					300					
tca	gat	gcc	tgg	cct	ctg	atg	cag	aat	ccc	atg	ggt	ggt	gac	aac	atc	960
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310					315					320	
tct	ttt	tgt	gac	tct	tat	cct	gaa	ctc	gct	gga	gaa	gac	att	cat	tct	1008
Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Ala	Gly	Glu	Asp	Ile	His	Ser	
				325					330					335		
ctc	aat	cca	gaa	ctt	gaa	agc	tca	acg	tct	ttg	gat	tca	aat	agc	agt	1056
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	
			340					345					350			
caa	gat	ttg	gtt	ggt	ggg	gct	gtt	cca	gtc	cag	tct	cat	tct	gaa	aac	1104
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	

355	360	365	
ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa			1152
Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu			
370	375	380	
tca gca tca act cag gat gca cta act atg aga agc cag cta gat cag			1200
Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln			
385	390	395	400
gag agt ggc gct atc atc cac cca gcc act cag acg tcc ctc cag gta			1248
Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val			
	405	410	415
agg cag cga ctg ggt tcc ctg tgaacacagc actgacttac agtagatcag			1299
Arg Gln Arg Leu Gly Ser Leu			
420			
aactctgttc ccagcataag atttgg			1325
<210> 4			
<211> 423			
<212> PRT			
<213> Homo sapiens			
<400> 4			
Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu			
1	5	10	15
Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly			
	20	25	30
Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro			
	35	40	45
Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe			
	50	55	60
Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe			
	65	70	75
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala			
	85	90	95
Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala			
	100	105	110
Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val			
	115	120	125
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro			
	130	135	140
Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser			
145	150	155	160

Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
 165 170 175
 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
 180 185 190
 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
 195 200 205
 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
 210 215 220
 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
 225 230 235 240
 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
 245 250 255
 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
 260 265 270
 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
 275 280 285
 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
 290 295 300
 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
 305 310 315 320
 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Ala Gly Glu Asp Ile His Ser
 325 330 335
 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
 340 345 350
 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
 355 360 365
 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
 370 375 380
 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
 385 390 395 400
 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val
 405 410 415
 Arg Gln Arg Leu Gly Ser Leu
 420

<210> 5
 <211> 1914
 <212> DNA
 <213> Mus musculus

<220>

<221> CDS

<222> (1)..(1248)

<400> 5

atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc	48
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala	
1 5 10 15	
att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga	96
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly	
20 25 30	
gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc	144
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu	
35 40 45	
tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc	192
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
50 55 60	
ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc	240
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe	
65 70 75 80	
aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg	288
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala	
85 90 95	
ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct	336
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala	
100 105 110	
gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt	384
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val	
115 120 125	
ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc	432
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro	
130 135 140	
tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc	480
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser	
145 150 155 160	
acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt	528
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser	
165 170 175	
gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac	576
Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr	
180 185 190	
tgc aag agg cag ttc atg gag aag aaa ccc agc tgg tct ctg cgg tca	624
Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser	
195 200 205	

cag gac att cag tac aat ggc tct gag ctg tca tgc ttt gac cag cct	672
Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Gln Pro	
210 215 220	
cgg ctc cgc cac tgt gcc cat aga gca tgc tgt cag tat cac cgg gac	720
Arg Leu Arg His Cys Ala His Arg Ala Cys Cys Gln Tyr His Arg Asp	
225 230 235 240	
tca gcc cca atg tat ggg cct gtt cac ctg att ccg tcc ttg tgc tgt	768
Ser Ala Pro Met Tyr Gly Pro Val His Leu Ile Pro Ser Leu Cys Cys	
245 250 255	
gaa gag gcc cgc agc tct gcc cga gct gtg ctt ggc tgt ggg ctg cgt	816
Glu Glu Ala Arg Ser Ser Ala Arg Ala Val Leu Gly Cys Gly Leu Arg	
260 265 270	
tct ccc act acc ctc cag gag aga aac ccg gct tct gtg ggg gac acg	864
Ser Pro Thr Thr Leu Gln Glu Arg Asn Pro Ala Ser Val Gly Asp Thr	
275 280 285	
atg cca gcc ttc ttc ggg tct gtt tcc cgt tcc atc tgc gct gaa ttt	912
Met Pro Ala Phe Phe Gly Ser Val Ser Arg Ser Ile Cys Ala Glu Phe	
290 295 300	
tct gat gcc tgg cct ctg atg cag aat cct ctg ggt ggt gac agc tct	960
Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Leu Gly Gly Asp Ser Ser	
305 310 315 320	
ctc tgt gac tct tat cct gaa ctc act gga gaa gat acc aat tcc ctc	1008
Leu Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Thr Asn Ser Leu	
325 330 335	
aat ccc gaa aac gaa agc gca gca tct ctg gat tcc agt ggc ggc cag	1056
Asn Pro Glu Asn Glu Ser Ala Ala Ser Leu Asp Ser Ser Gly Gly Gln	
340 345 350	
gat ctg gct ggg aca gct gct cta gag tct tct ggg aat gtt tca gaa	1104
Asp Leu Ala Gly Thr Ala Ala Leu Glu Ser Ser Gly Asn Val Ser Glu	
355 360 365	
tct act gac tca cct aga cat ggt gac act ggt aca gtc tgg gag cag	1152
Ser Thr Asp Ser Pro Arg His Gly Asp Thr Gly Thr Val Trp Glu Gln	
370 375 380	
acg cta gct cag gat gct caa agg act cca agc caa gga ggc tgg gaa	1200
Thr Leu Ala Gln Asp Ala Gln Arg Thr Pro Ser Gln Gly Gly Trp Glu	
385 390 395 400	
gac agg gaa aac ctg aat cta gcc atg ccc aca gcc ttc cag gat gcc	1248
Asp Arg Glu Asn Leu Asn Leu Ala Met Pro Thr Ala Phe Gln Asp Ala	
405 410 415	
tgaaggccat cttcctgacg tggaggtgtg ggtctggaca agcctgtgat gaggcctaca	1308
gactgagcag tcttggtgtc tggaagcaaa aataaatctg aaccaaactg acaacatttc	1368
catcctttca gccactagct tctgagccag accagctgta agctgaaacc ccagcaagaa	1428

gcaaggagag actgactgta ggcggccttg ggacatgtgc ttcttccta agcgagaacc 1488
ttagctgggg ccaatttgaa ggacccatgg gtggaatgtg ctgcctgtga gcttgtgggc 1548
acagcaggac ccagcctggc tccttcttat gtccacgggtg aatgtgggtt cacaagaccc 1608
agagtataaa ctttcataga cattctcttt tagaaataat ccattaccct gtcttcaaaa 1668
acaaaaaaaa aaaaaaagtg gtgttaaggt tttgaacatc acctagccaa gttagtaaaa 1728
tctttatttg tatttcatct caattttttt aactattcat tttccttgta tgaattcttg 1788
tgtgttttat gtgtaaatat attcattatt ttgacactat caatattctt tgtgggtttg 1848
taatttttac ttttattaat gactcaagct gtaaaaataa actaatttca acgtcgacgc 1908
ggccgc 1914

<210> 6
<211> 416
<212> PRT
<213> Mus musculus

<400> 6
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
20 25 30
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
35 40 45
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
50 55 60
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
65 70 75 80
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
85 90 95
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
100 105 110
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
115 120 125
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
130 135 140
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser
145 150 155 160
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser

165							170							175						
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr					
			180					185					190							
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser					
		195					200					205								
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Gln	Pro					
	210					215					220									
Arg	Leu	Arg	His	Cys	Ala	His	Arg	Ala	Cys	Cys	Gln	Tyr	His	Arg	Asp					
225					230				235						240					
Ser	Ala	Pro	Met	Tyr	Gly	Pro	Val	His	Leu	Ile	Pro	Ser	Leu	Cys	Cys					
			245						250					255						
Glu	Glu	Ala	Arg	Ser	Ser	Ala	Arg	Ala	Val	Leu	Gly	Cys	Gly	Leu	Arg					
			260					265					270							
Ser	Pro	Thr	Thr	Leu	Gln	Glu	Arg	Asn	Pro	Ala	Ser	Val	Gly	Asp	Thr					
		275					280					285								
Met	Pro	Ala	Phe	Phe	Gly	Ser	Val	Ser	Arg	Ser	Ile	Cys	Ala	Glu	Phe					
	290					295					300									
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Leu	Gly	Gly	Asp	Ser	Ser					
305					310					315					320					
Leu	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Thr	Asn	Ser	Leu					
			325						330					335						
Asn	Pro	Glu	Asn	Glu	Ser	Ala	Ala	Ser	Leu	Asp	Ser	Ser	Gly	Gly	Gln					
			340					345					350							
Asp	Leu	Ala	Gly	Thr	Ala	Ala	Leu	Glu	Ser	Ser	Gly	Asn	Val	Ser	Glu					
		355					360					365								
Ser	Thr	Asp	Ser	Pro	Arg	His	Gly	Asp	Thr	Gly	Thr	Val	Trp	Glu	Gln					
	370					375					380									
Thr	Leu	Ala	Gln	Asp	Ala	Gln	Arg	Thr	Pro	Ser	Gln	Gly	Gly	Trp	Glu					
385					390					395					400					
Asp	Arg	Glu	Asn	Leu	Asn	Leu	Ala	Met	Pro	Thr	Ala	Phe	Gln	Asp	Ala					
			405						410					415						

<210> 7
 <211> 27
 <212> DNA
 <213> Mus musculus

<400> 7
 aggccatctt cctgacgtgg aggtgtg

<210> 8
 <211> 35
 <212> DNA
 <213> Mus musculus

<400> 8
 cggaattcgt ttcagctcag cacattccaa ggccg

35

<210> 9
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 9
 Ser Thr Ala Ser Ser Pro Arg Asp Thr
 1 5

<210> 10
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 10
 Asp Lys Thr His Thr Cys Pro
 1 5

<210> 11
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
 1 5 10 15
 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
 20 25 30
 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
 35 40 45
 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
 65 70 75 80
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
 85 90 95
 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
 100 105 110
 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125

Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
130						135					140					
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
				165					170					175		
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Arg	Pro	
210						215					220					
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230				235						240	
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245					250					255		
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
			260					265					270			
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
290						295					300					
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310					315					320	
Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	Ser	
				325					330					335		
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	
			340					345					350			
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	
		355					360					365				
Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu	
370						375					380					
Ser	Ala	Ser	Thr	Gln	Asp	Ala	Leu	Thr	Met	Arg	Ser	Gln	Leu	Asp	Gln	
385					390					395					400	
Glu	Ser	Gly	Ala	Val	Ile	His	Pro	Ala	Thr	Gln	Thr	Ser	Leu	Gln	Glu	
				405				410						415		

Ala

<210> 12
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
 1 5 10 15
 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
 20 25 30
 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
 35 40 45
 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Ala Cys Arg Leu His Arg Phe
 65 70 75 80
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
 85 90 95
 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
 100 105 110
 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140
 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
 145 150 155 160
 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
 165 170 175
 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
 180 185 190
 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
 195 200 205
 Gln Asp Ile Gln Tyr Asn Glu Ser Glu Leu Ser Cys Phe Asp Arg Pro
 210 215 220
 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
 225 230 235 240
 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
 245 250 255
 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His

260	265	270
Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met		
275	280	285
Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe		
290	295	300
Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile		
305	310	315 320
Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser		
	325	330 335
Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser		
	340	345 350
Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn		
	355	360 365
Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu		
	370	375 380
Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln		
385	390	395 400
Glu Ser Gly Ala Val Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu		
	405	410 415
Arg Gln Arg Leu Gly Ser Leu		
	420	

<210> 13
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Consensus
 sequence

<400> 13
Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu
1 5 10 15
Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
20 25 30
Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
35 40 45
Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
50 55 60
Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
65 70 75 80

Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys	Pro	Cys	Leu	Asp	Cys	Ala	
				85					90					95		
Val	Val	Asn	Arg	Phe	Gln	Lys	Ala	Asn	Cys	Ser	Ala	Thr	Ser	Asp	Ala	
			100					105					110			
Ile	Cys	Gly	Asp	Cys	Leu	Pro	Gly	Phe	Tyr	Arg	Lys	Thr	Lys	Leu	Val	
		115					120					125				
Gly	Phe	Gln	Asp	Met	Glu	Cys	Val	Pro	Cys	Gly	Asp	Pro	Pro	Pro	Pro	
	130					135					140					
Tyr	Glu	Pro	His	Cys	Ala	Ser	Lys	Val	Asn	Leu	Val	Lys	Ile	Ala	Ser	
145					150					155					160	
Thr	Ala	Ser	Ser	Pro	Arg	Asp	Thr	Ala	Leu	Ala	Ala	Val	Ile	Cys	Ser	
				165					170					175		
Ala	Leu	Ala	Thr	Val	Leu	Leu	Ala	Leu	Leu	Ile	Leu	Cys	Val	Ile	Tyr	
			180					185					190			
Cys	Lys	Arg	Gln	Phe	Met	Glu	Lys	Lys	Pro	Ser	Trp	Ser	Leu	Arg	Ser	
		195					200					205				
Gln	Asp	Ile	Gln	Tyr	Asn	Gly	Ser	Glu	Leu	Ser	Cys	Phe	Asp	Arg	Pro	
	210					215					220					
Gln	Leu	His	Glu	Tyr	Ala	His	Arg	Ala	Cys	Cys	Gln	Cys	Arg	Arg	Asp	
225					230				235						240	
Ser	Val	Gln	Thr	Cys	Gly	Pro	Val	Arg	Leu	Leu	Pro	Ser	Met	Cys	Cys	
				245					250					255		
Glu	Glu	Ala	Cys	Ser	Pro	Asn	Pro	Ala	Thr	Leu	Gly	Cys	Gly	Val	His	
			260					265					270			
Ser	Ala	Ala	Ser	Leu	Gln	Ala	Arg	Asn	Ala	Gly	Pro	Ala	Gly	Glu	Met	
		275					280					285				
Val	Pro	Thr	Phe	Phe	Gly	Ser	Leu	Thr	Gln	Ser	Ile	Cys	Gly	Glu	Phe	
	290					295					300					
Ser	Asp	Ala	Trp	Pro	Leu	Met	Gln	Asn	Pro	Met	Gly	Gly	Asp	Asn	Ile	
305					310					315					320	
Ser	Phe	Cys	Asp	Ser	Tyr	Pro	Glu	Leu	Thr	Gly	Glu	Asp	Ile	His	Ser	
				325					330					335		
Leu	Asn	Pro	Glu	Leu	Glu	Ser	Ser	Thr	Ser	Leu	Asp	Ser	Asn	Ser	Ser	
			340					345					350			
Gln	Asp	Leu	Val	Gly	Gly	Ala	Val	Pro	Val	Gln	Ser	His	Ser	Glu	Asn	
		355					360					365				
Phe	Thr	Ala	Ala	Thr	Asp	Leu	Ser	Arg	Tyr	Asn	Asn	Thr	Leu	Val	Glu	
	370					375					380					

Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
 385 390 395 400

Glu Ser Gly Ala Ile His Pro Ala Thr Gln Thr Ser Leu Gln Gln Arg
 405 410 415

Leu Gly Ser Leu
 420

<210> 14
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 14
 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
 1 5 10 15

Ala

<210> 15
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 15
 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val
 1 5 10 15

Arg Gln Arg Leu Gly Ser Leu
 20

<210> 16
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 16
 Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys
 1 5 10 15

Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val
 20 25 30

Cys Glu

<210> 17
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 17

Cys Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg
1 5 10 15

Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val
20 25 30

Cys Arg

<210> 18

<211> 35

<212> PRT

<213> Homo sapiens

<400> 18

Cys Arg Glu Lys Gln Tyr Leu Leu Asn Ser Gln Cys Cys Ser Leu Cys
1 5 10 15

Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu Thr
20 25 30

Glu Cys Leu
35

<210> 19

<211> 40

<212> PRT

<213> Homo sapiens

<400> 19

Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro Cys
1 5 10 15

Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly
20 25 30

Tyr Gly Glu Asp Ala Gln Cys Val
35 40

<210> 20

<211> 42

<212> PRT

<213> Homo sapiens

<400> 20

Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr Glu
1 5 10 15

Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser Ala
20 25 30

Pro Cys Val Glu Ala Asp Asp Ala Val Cys

35

40

<210> 21
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 21
 Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro Cys
 1 5 10 15
 Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys Gln
 20 25 30
 Leu Cys Thr Ala Thr Gln Asp Thr Val Cys
 35 40

<210> 22
 <211> 43
 <212> PRT
 <213> Homo sapiens

<400> 22
 Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His
 1 5 10 15
 Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln
 20 25 30
 Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys
 35 40

<210> 23
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 23
 Thr Cys Arg Leu His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys
 1 5 10 15
 Lys Pro Cys Leu Asp Cys Ala Val Val Asn Arg Phe Gln Lys Ala Asn
 20 25 30
 Cys Ser Ala Thr Ser Asp Ala Ile Cys
 35 40

<210> 24
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 24

Asp Lys Thr His Thr Cys Pro
1 5

Al
cancel